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FIG. 1

5'	9				18				27				36				45				54			
	CAG	CCC	CGG	GGC	GCC	GGC	CGC	GCG	CAG	CCT	CGC	TAT	CCC	ACC	CAG	GCT	CCG	GGC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	63				72				81				90				99				108			
	TTC	CAG	GAG	GGT	CGC	GGA	GCC	CCA	AGC	CAT	GAC	TAA	GGA	GCC	CAT	TTG	ATA	GCA						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	117				126				135				144				153				162			
	GAG	GTG	GCG	CGC	AGC	CCG	GCG	AGC	CGA	TGA	CGG	ACC	CCT	TCT	TCC	TGC	CTT	CAA						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	171				180				189				198				207				216			
	TGC	CTC	AGC	GGA	AGA	TCC	CCA	AGG	GCT	GGA	GCG	AGG	AGC	GCT	GCC	GCT	GGA	CAT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	225				234				243				252				261				270			
	CCT	CCC	GGG	GAG	GCT	GCT	CCG	ACC	TGC	TGC	GCG	GCG	CGT	CTG	AGA	CTG	GGG	ACT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	279				288				297				306				315				324			
	GAG	CCA	CTC	CGC	CGC	CGC	CGG	CGC	CGC	CGC	CGC	CGC	CCG	CTC	CGT	CGC	TGC	CGT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	333				342				351				360				369				378			
	CGG	TCT	GGA	CTG	GCC	CCC	ACC	TCG	CTG	CGC	CCT	CTC	CCC	GGC	CCC	GGC	CCC	GGC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	387				396				405				414				423				432			
	TCG	GGG	CGT	CCC	GGG	GCT	CGC	CCT	GCG	ACC	GCC	GCC	TCC	CGC	GCG	CCG	CGT	CCT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	441				450				459				468				477				486			
	CCC	GAC	CCC	GCG	GCG	GCG	ACG	ATG	CCC	GGG	AGG	AGG	GTC	CTG	ACG	GCG	GCG	GCG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	495				504				513				522				531				540			
	CGG	ATG	GTG	GCG	GCC	GGC	GCC	CGG	GTG	TGA	TGC	GAG	CGT	CAC	GGT	GGG	GAT	GCT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	549				558				567				576				585				594			
	GCT	GGC	TGC	GCG	GCG	CTG	AGG	GCC	AGC	GAG	AGC	GAG	AGC	CCG	CCC	GGG	GCG	GAG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	603				612				621				630				639				648			
	GAC	GGA	CTC	ATC	CGG	ATC	TGG	CTG	CAG	CGT	GGG	CTC	GGA	GCT	CCC	CCT	TCC	TCT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	657				666				675				684				693				702			
	CGG	TCT	CCC	TCT	CGG	CCC	CCC	TTT	ATT	TCC	TTC	TTG	CTT	TGC	GTC	TTT	AAC	ACC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	711				720				729				738				747				756			
	TCT	CGA	CCC	TGT	CCT	CCC	CCC	GCC	ACT	GGA	AGT	CTT	CCC	GTC	TCT	AAA	TGG	AAT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	765				774				783				792				801				810			
	TAG	TGG	AGC	CCG	GAG	CCT	CTG	GTG	TAA	CGC	ACA	GAC	ATG	ATC	CAT	GGG	CGC	AGC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
													M	I	H	G	R	S						
	819				828				837				846				855				864			
	GTG	CTT	CAC	ATT	GTA	GCA	AGT	TTA	ATC	ATC	CTC	CAT	TTG	TCT	GGG	GCA	ACC	AAG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	V	L	H	I	V	A	S	L	I	I	L	H	L	S	G	A	T	K						
	873				882				891				900				909				918			
	AAA	GGA	ACA	GAA	AAG	CAA	ACC	ACC	TCA	GAA	ACA	CAG	AAG	TCA	GTG	CAG	TGT	GGA						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
	K	G	T	E	K	Q	T	T	S	E	T	Q	K	S	V	Q	C	G						

927 936 945 954 963 972
ACT TGG ACA AAA CAT GCA GAG GGA GGT ATC TTT ACC TCT CCC AAC TAT CCC AGC
T W T K H A E G G I F T S P N Y P S

981 990 999 1008 1017 1026
AAG TAT CCC CCT GAC CGG GAA TGC ATC TAC ATC ATA GAA GCC GCT CCA AGA CAG
K Y P P D R E C I Y I I E A A P R Q

1035 1044 1053 1062 1071 1080
TGC ATT GAA CTT TAC TTT GAT GAA AAG TAC TCT ATT GAA CCG TCT TGG GAG TGC
C I E L Y F D E K Y S I E P S W E C

1089 1098 1107 1116 1125 1134
AAA TTT GAT CAT ATT GAA GTT CGA GAT GGA CCT TTT GGC TTT TCT CCA ATA ATT
K F D H I E V R D G P F G F S P I I

1143 1152 1161 1170 1179 1188
GGA CGT TTC TGT GGA CAA CAA AAT CCA CCT GTC ATA AAA TCC AGT GGA AGA TTT
G R F C G Q Q N P P V I K S S G R F

1197 1206 1215 1224 1233 1242
CTA TGG ATT AAA TTT TTT GCT GAT GGA GAG CTG GAA TCT ATG GGA TTT TCA GCT
L W I K F F A D G E L E S M G F S A

1251 1260 1269 1278 1287 1296
CGA TAC AAT TTC ACA CCT GGT AAG TAA GTA CTT AAA AAA AAA ATT TCT TTT TCT
R X N F T P G K *

1305 1314 1323 1332 1341 1350
TCC TCA TTT TTC TAT CTT CAT AGT ACA AAA TCT TGT GTA AGA CAA CAT TAT ACT
TTC TCA GAG AAT GTT CCA GTT CTA TTT AAA ACC AAA TCT ACA GTG CTT TTT CTT
1413 1422 1431 1440 1449 1458
TTC CCT ACA CAA ATT CTG AAA GGA AAA GAT GTT TTC CTT AAA ACA GCC TAT ACT
1467 1476 1485 1494 1503 1512
AGA GGT AAA GAG TAG TGA CTC AAG GCT CTA AAT GGG CAT CAG CCA CAT CAT CAA
1521 1530 1539 1548 1557 1566
GTG GAC TTT TGT TAT GAT GGA ATG TGT AAT TGG AGA GAC AGT CTG TGA TAA GGA
1575 1584 1593 1602 1611 1620
AAC TAT ACA TAG GAG CTG AAT AAA CTT GAA AAG ACA ATT GTA GTA TTA TAA AAT
1629 1638 1647 1656 1665 1674
ATA TCC ACC AAA ATG ATC TTT GGG GAA CTT GAA TCA AAA GTT TAT TTG TTC TGA
1683 1692 1701 1710 1719 1728
AAA TTA CCG TGT TTC AAT CAA ATA GAT CCT ACT TTA GGA AGT AGT CTG CTC TCT
1737 1746 1755 1764 1773 1782
TTT CAG GAA AGC AAA TTC TTA AGA GTT TTG ATG AAA GGA AAA CTG AGA CCT GTA

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1791	1800	1809	1818	1827	1836
ACA GCC AAA TAC TCA TTT ACA AGG TCT TGC AGA AAT TGT GTG CAA TTA TCA AAT					

1845	1854	1863	1872	1881	1890
TAT GCA ATC TGT ATC AAT TTT CCT TTT AAC TCG CTA GAA TTA AAA AGA TCC TGT					

1899	1908	1917	1926	1935	1944
GTT GTT GCC TGG CCC ACT TGA TTA AGA GTT ACC ATT CAT TAC AAT AAA AAT AGG					

1953	1962	1971	1980	1989	1998
TTA TCA CAT TTT TTC ACT GCA AGA ACA CTA CAT GCA TTA ATT TAA ATG GAA AAA					

2007	2016	2025	2034	2043	2052
TGA TTC AAA TTA CAT AAA GCC CAT TTT TTA TAT AGT TTG TTT TCA GTT TGT ATG					

2061	2070	2079	2088	2097	2106
TAT TGT TTT ATT TAA GTT AGG CAA TAG CAT AAT TTC AAA TAT ATG TAA AGT TGG					

2115	2124	2133	2142	2151	2160
TTG AAG TTT GTA TTC CAT GTT AAA GAA GTA ACA TCT AAA TAC AGC TTT GAT ACT					

2169	2178	2187	2196	2205	2214
CAG TTA AAA AAC TAA AAT TTT AAA AAT TAT TAA TAT AAG TTT AAT GAT GAC TTT					

2223	2232	2241	2250	2259	2268
CAT TAT GAC ATC ATG GGG TAT GTT AAA TCA AGT ATT TAC TGT AGC ATA TAT ATT					

2277	2286	2295	2304	2313	2322
AGC TTT AAG CAT TAG GAA TGT TTT TAA TAA TAT CAC TAA AGG ATT GTG GTT TTA					

2331	2340	2349	2358	2367	2376
ATT ATG CTT TGC TGA TAA TGG ATT ACT CAC AGA AAT CAT GGG TAT TTC ATG TGC					

2385	2394	2403	2412	2421	2430
TAC AGT CGA ACT AAT TTG AAG TAT TCC CAA AAG GTA CAA ATG TTA GCT TAA TTT					

2439	2448	2457	2466	2475	2484
GTT TGT TCA GAT TAT TAG TGC TAG AGT TGT AAA TGG AAA GGT AGG TAT TTT TTT					

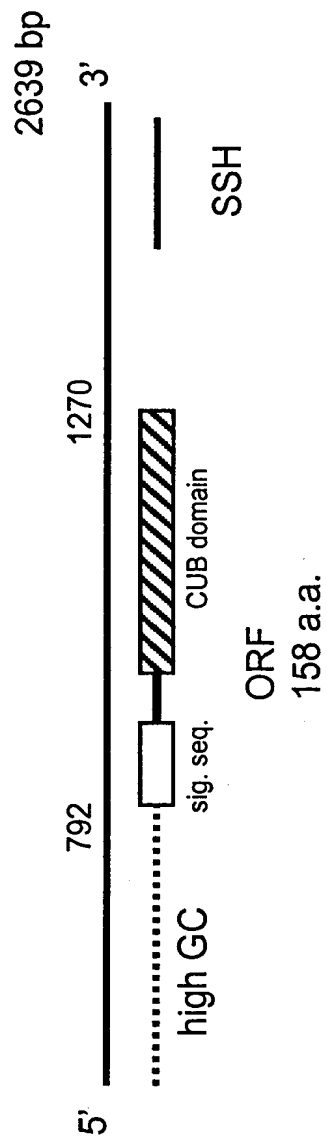
2493	2502	2511	2520	2529	2538
CTT AAC TGA TAA TTT TGA ATA TAA CCT GTA CCT AGA GAC AGT GAC ATA CGG CAT					

2547	2556	2565	2574	2583	2592
GTT CTA GGT TTC ATA AGT TAT ATT TTC ATT CTG GGT TTG GTG ATC ATG AAA ATA					

2601	2610	2619	2628	2637	
ATG TCT TGG ATT TAA AAT TGT GGT TTC ACA AAA AAA AAA AAA AAA AA 3'					

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FIG. 2



GC content:	
5' non-coding	72%
coding	42%
3' non-coding	30%

0903593-06P107

43.5% identity in 115 residues overlap

B

35.3% identity in 102 residues overlap in CUB domain 1 of BMP-1

BPC-1 130 GIFTSPNYPSKYPPDRECIYIIIEAAPQRCIELYFDEKYSIEPSWECKFDHIEVRDGPFGF
BMP-1 336 GNFSSPEYPNGYSAHMCVWRISVTPEKII LNFTSM-DLYRSRLCWYDYVEVRDGFWRK

BPC-1 190 SPIIGRF~~C~~Q~~Q~~NPPVIKSSGRFLWIKFFADGELES~~M~~GFSARY
BMP-1 395 VWVRGRF~~C~~GGKLPEPIVSTDSRLWVEFRSSSNWVGKGF~~F~~AVY
***** * * * ** * *

39.4% identity in 104 residues overlap in CUB domain 2 of BMP-1

BPC-1 128 EGGIFTSPNYPSPKYPDPDRECIYIIIEAAPRQCIELYFDEKYSIEPSWECKFDHIEVRDGGPF
BMP-1 447 DNGHIQSPNYPDDYRPSKVCTWRIQVSEGFHVGLTF-QSFIEIRHDSCAYDYLVLEVRDGHs

BPC-1 188 GFSP IIGRF CGQNP PVIKSSGRFLWIKFFADGELESMGFSARY
BMP-1 506 ESSNLIGRYCGYENPDDIKSTSSRLWLKFVSDGSINKAGFAVNF
* * * * *

36.3% identity in 102 residues overlap in CUB domain 3 of BMP-1

BPC-1 130 GIFTSPNYPYSKYPPDRECIYIIEAAPRQCIELYFDEKYSIEPSWECKFDHIEVRDGPFGF
BMP-1 605 GSITSPGPWKPEYPPKNKNCIQVLVAPTQYRISLQFDF-FETEGNDVCKYDFVEVRSGLTAD
* * * * * * * * * * * * * * * * * * * * * * * *

BPC-1 190 SPIIGRFCGQONPPVIKSSGRFLWIKFFADGELESMGFSARY
BMP-1 664 SKLHGKFCGSEKPEVITSQYNNMRVEFKSDNTVSKKGFKAHF
* * * * *

37.9% identity in 103 residues overlap in CUB domain 4 of BMP-1

BPC-1 130 GIFTSPNYPSKYPPDRECIYIIIEAAPRQCIELYFDEKYSIEPSWECKFDHIEVRDGPFGF
BMP-1 761 GTITSPNWDKYPYSKKECTWAISSTPGHRVKLTFVEM-DIESQPECAYDHLEVFDDGRDAK

* * * * *

BPC-1 190 SPIIGRFCGQQNPPVIKSSGRFLWIKFFADGELESMGFSARYN
BMP-1 820 APVLGRFCGSKKPEPVLATGNRMFLRFYSDNSVQRKGFQASHS
* * * * *

32.3% identity in 96 residues overlap in CUB domain 5 of BMP-1

BPC-1 139 SKYPFDRECIYIIIEAAPRQCIELYFDEKYSIEPSWECKFDHIEVRDGPFGFSPIIGRFCG
BMP-1 887 NNPYPGGVDCEWVIVAEEGYGVLEVF-QTFEVEEETDCGYDYIELFDGYDSTAPRLGRYCG
* * * * *
* * * * *

BPC-1 199 QQNPPVIKSSGRFLWIKFFADGELESMGFSARYNFT
BMP-1 946 SGPPEEVYSAGDSVLVKFHSDDTISKKGFLHRYTST
* * * * *

FIG. 4

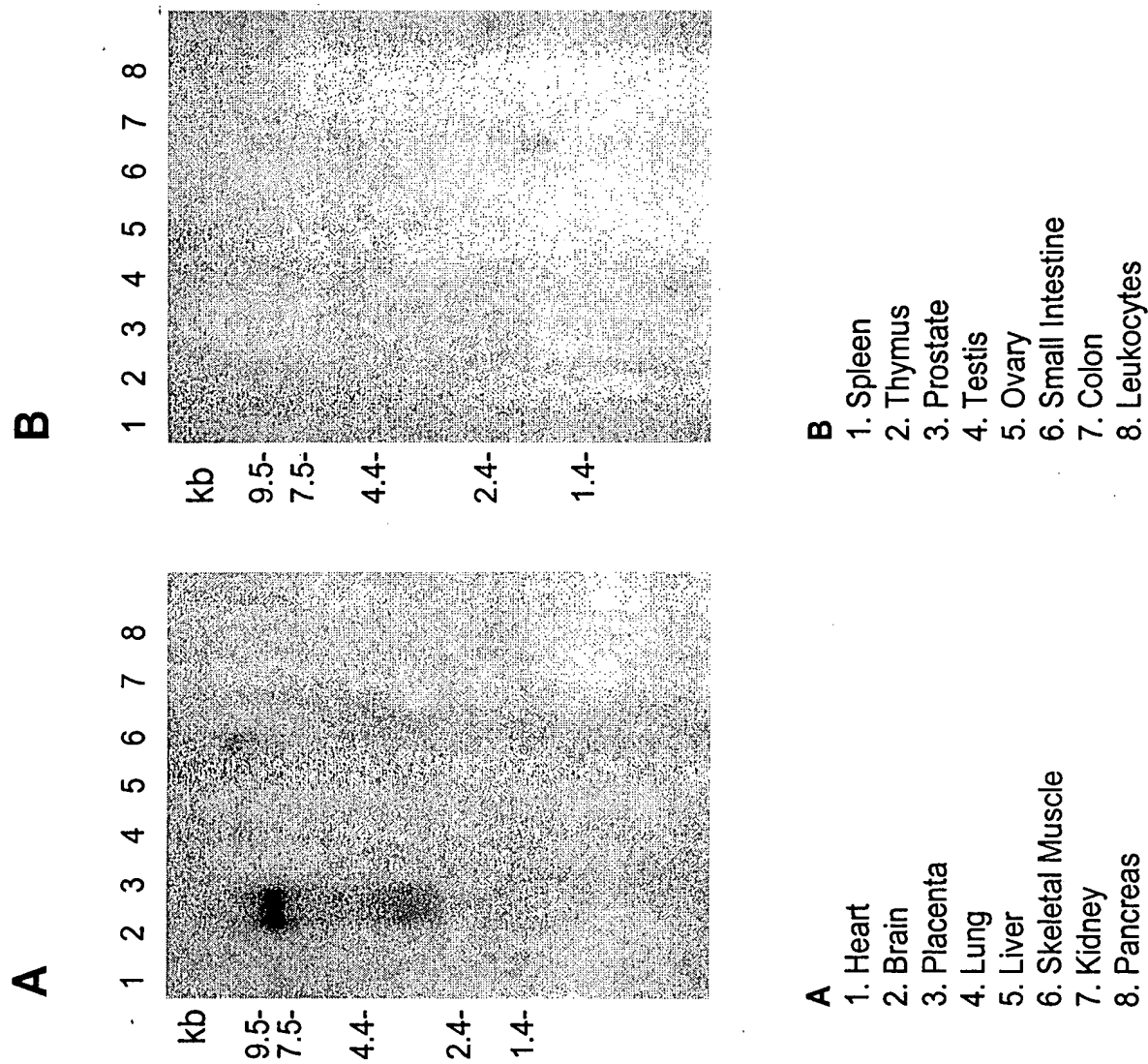
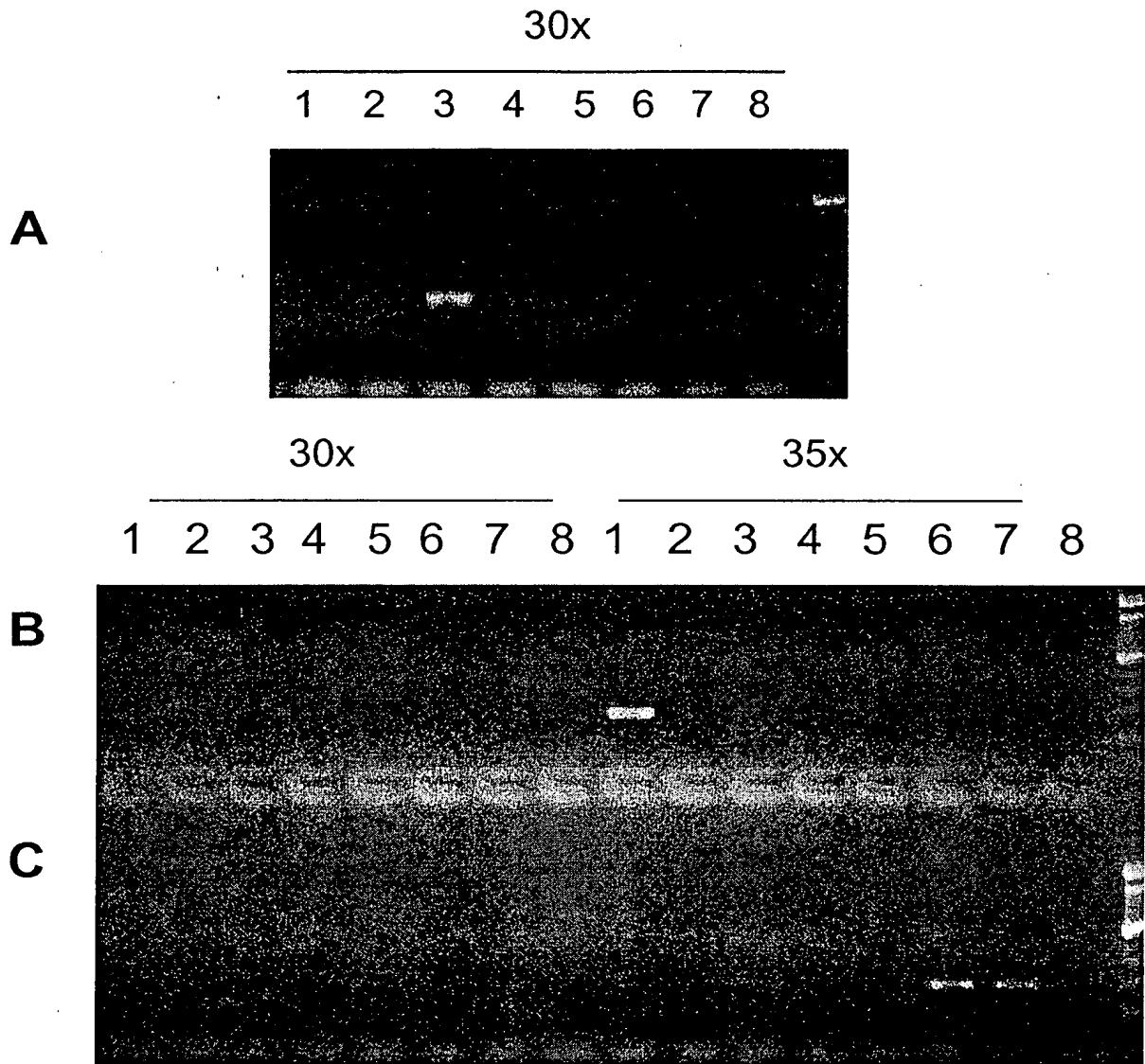


FIG. 5



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

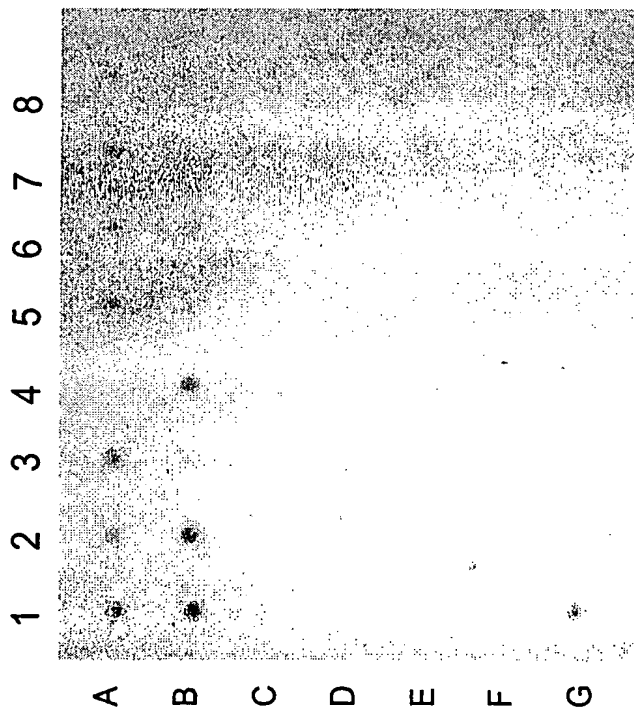
1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

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FIG. 6



A1 brain
A2 amygdala
A3 caudate nucleus
A4 cerebellum
A5 cerebral cortex
A6 frontal lobe
A7 hippocampus
A8 medulla oblongata

B1 occipital lobe
B2 putamen
B3 substantia nigra
B4 temporal lobe
B5 thalamus
B6 sub-thalamic nucleus
B7 spinal cord

C1 heart
C2 aorta
C3 skeletal muscle
C4 colon
C5 bladder
C6 uterus
C7 prostate
C8 stomach

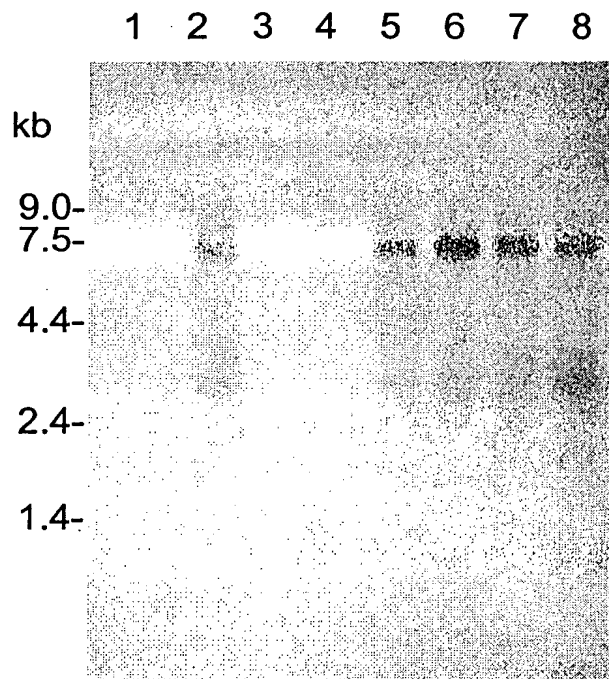
D1 testis
D2 ovary
D3 pancreas
D4 pituitary gland
D5 adrenal gland
D6 thyroid gland
D7 salivary gland
D8 mammary gland

E1 kidney
E2 liver
E3 small intestine
E4 spleen
E5 thymus
E6 peripheral leukocytes
E7 lymph node
E8 bone marrow

F1 appendix
F2 lung
F3 trachea
F4 placenta

G1 fetal brain
G2 fetal heart
G3 fetal kidney
G4 fetal liver
G5 fetal spleen
G6 fetal thymus
G7 fetal lung

FIG. 7

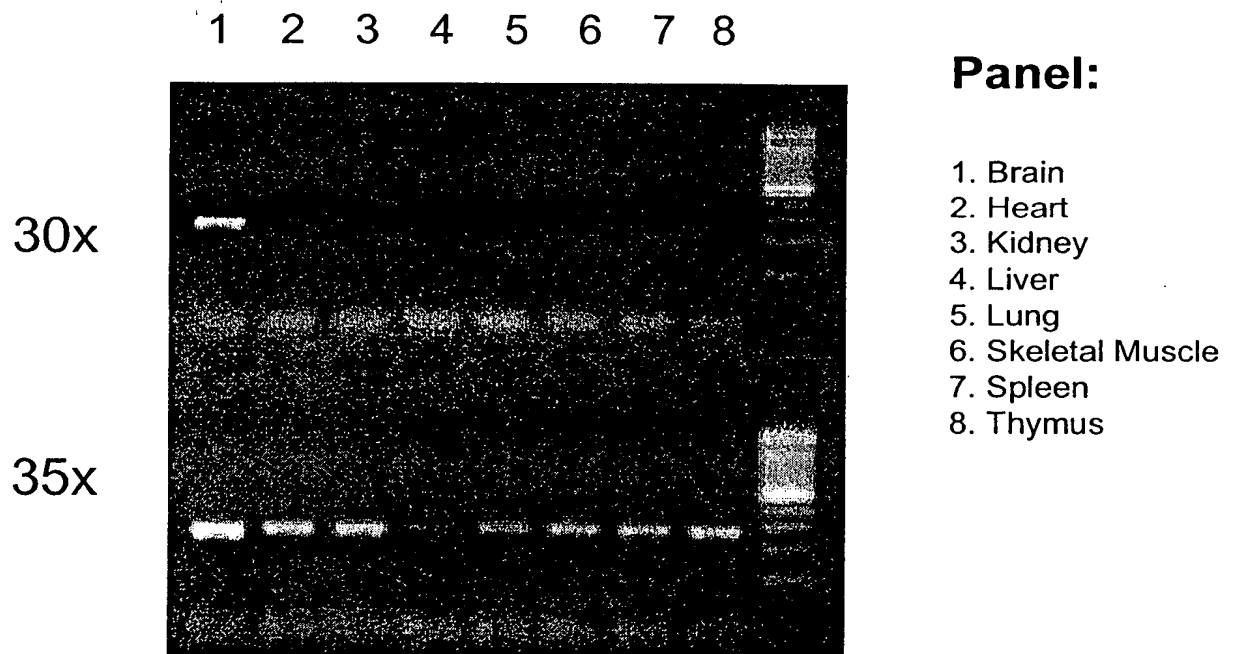


Lanes:

1. Cerebellum
2. Cerebral Cortex
3. Medulla
4. Spinal Cord
5. Occipital Lobe
6. Frontal Lobe
7. Temporal Lobe
8. Putamen

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T01290-66548860

FIG. 8



008750-665/8860

FIG. 9

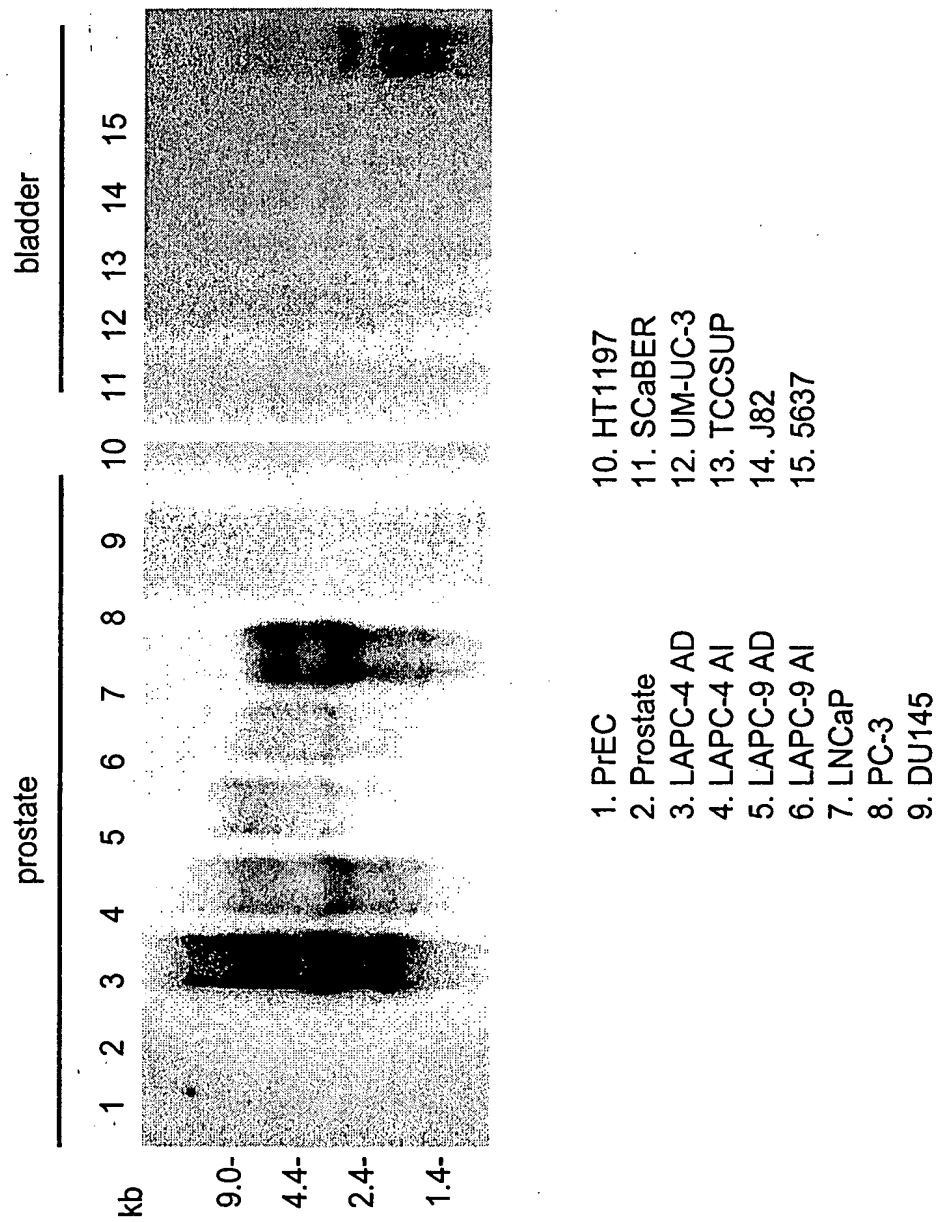


FIG. 10

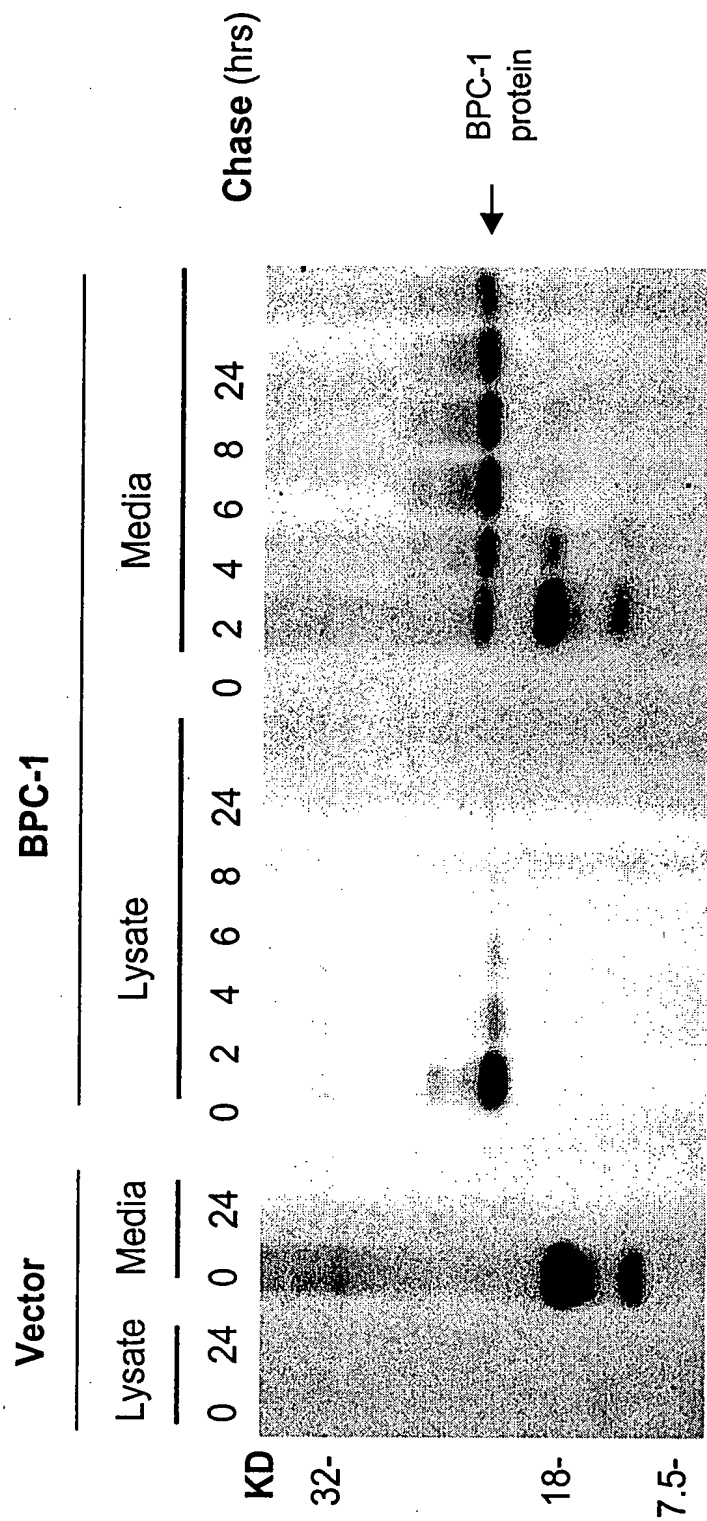
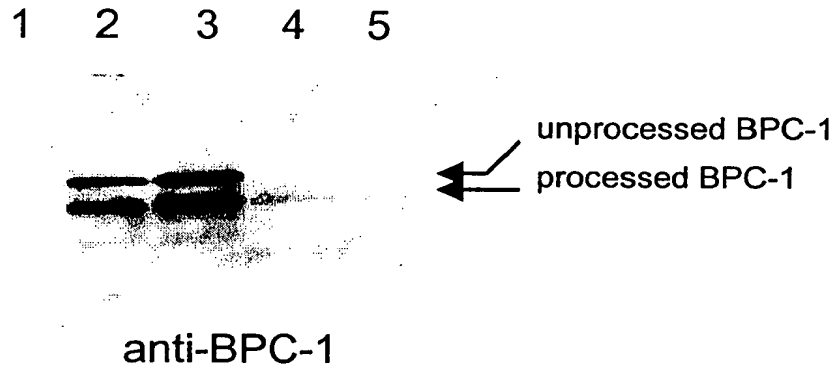


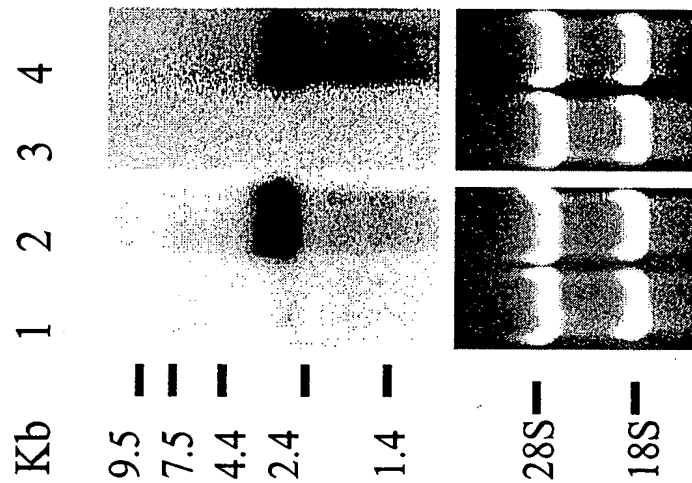
FIG. 11



Lanes:

1. HighFive cell extract- uninfected
2. HighFive cell extract- infected with BPC-1 virus
3. HighFive cell extract - infected with BPC-1 virus
4. HighFive cell media - infected with BPC-1 virus
5. HighFive cell media - infected with BPC-1 virus

FIG. 12



1. PC3/neo
2. PC3/BPC-1
3. 3T3CL7/neo, acute infection
4. 3T3CL7/BPC-1, acute infection

FIG. 13

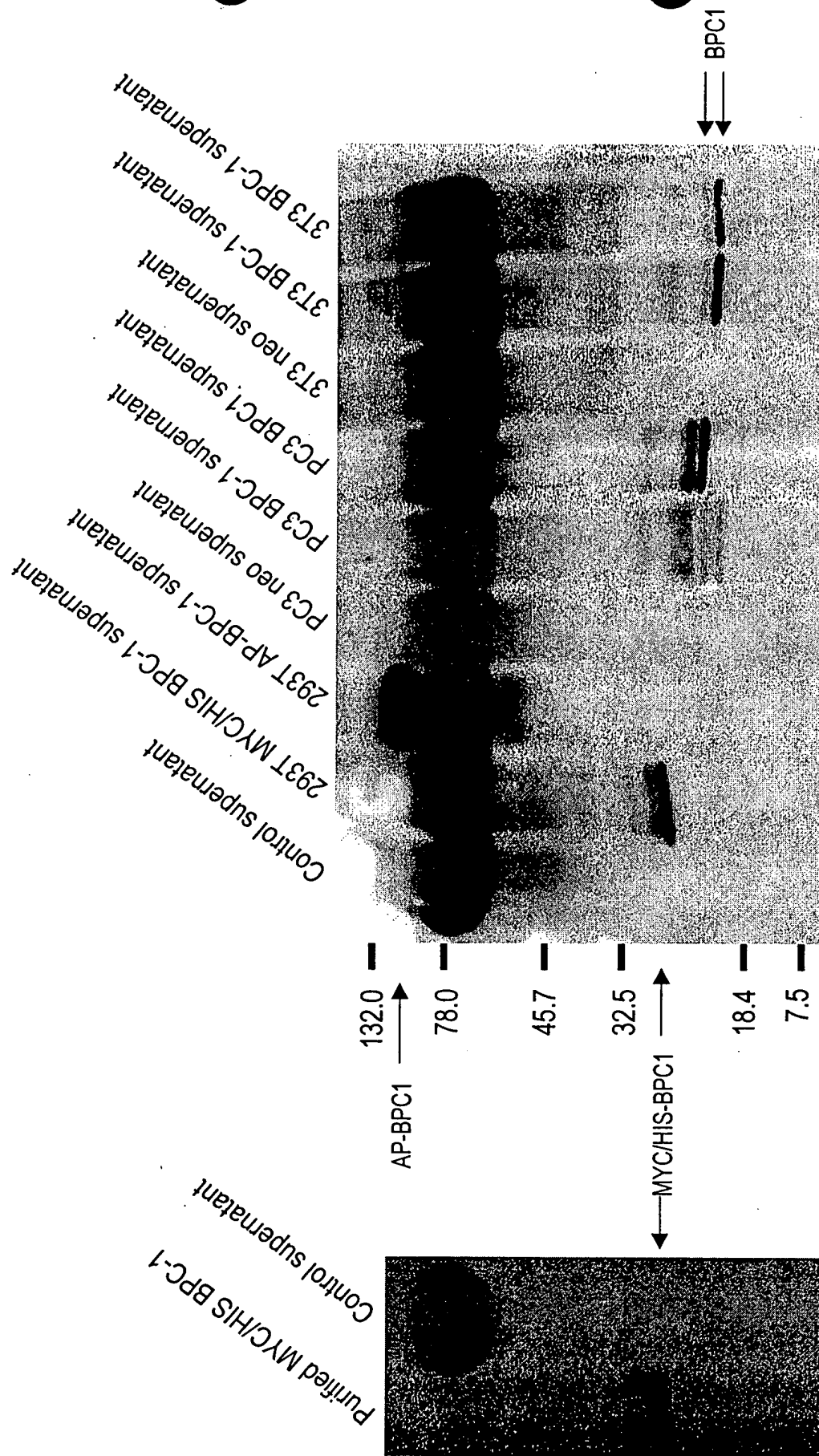
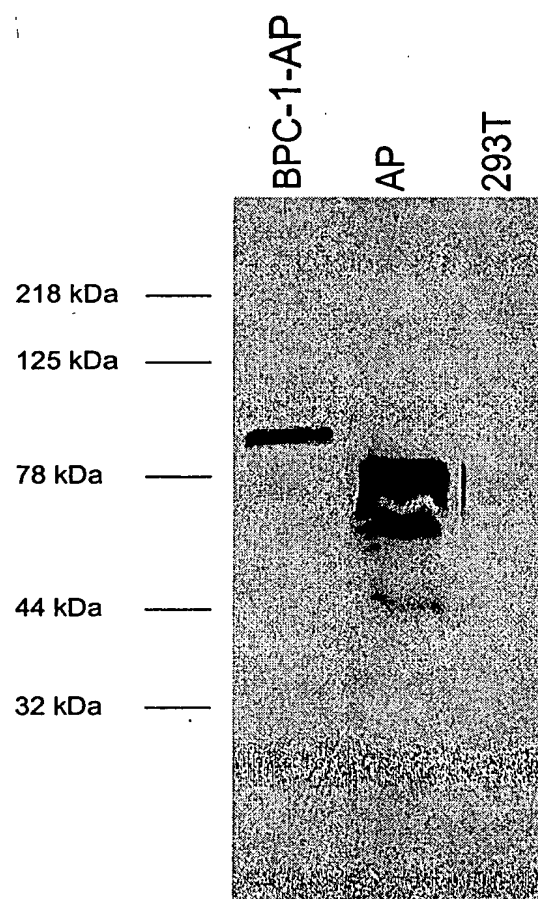


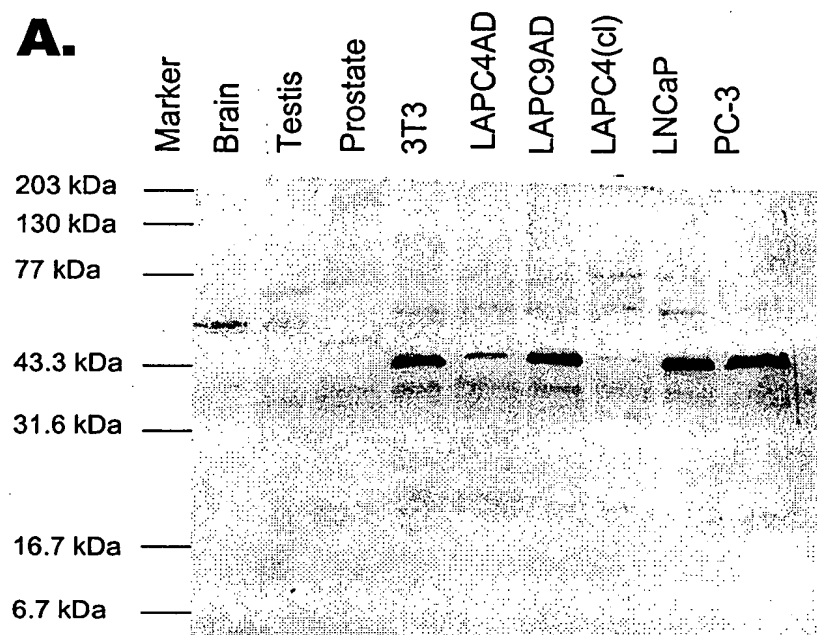
FIG. 14



Anti-HIS

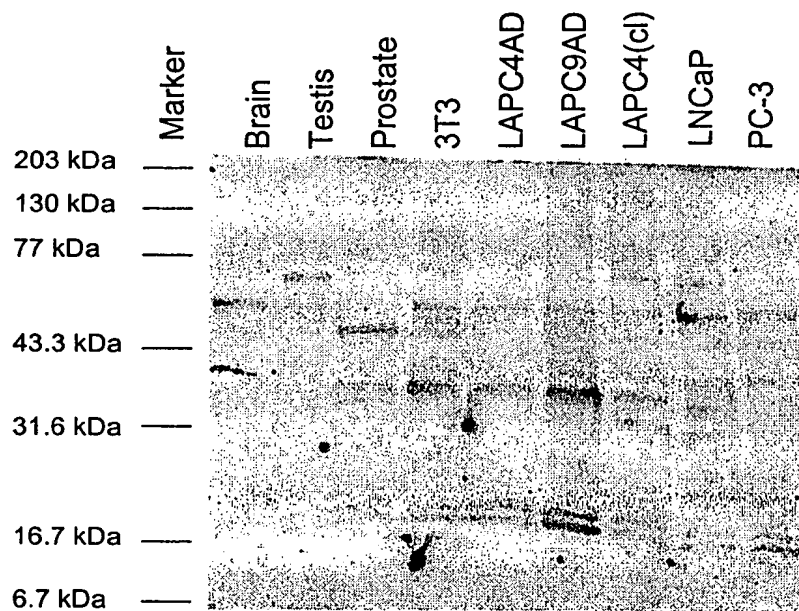
FIG. 15

A.



**BPC-1-AP
Conditioned Media**

B.



**Alkaline Phosphatase
Conditioned Media**

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